

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 22, 2002, 16:54:59 ; Search time 70.31 seconds

(without alignments)
54.090 Million cell updates/sec

Title: PCT-US01-32136-1

Perfect score: 151

Sequence: 1 ITLKYCYVTLKNGLDGVFYCHYN 26

Scoring table: BLOSUM62

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	76.2	338	12 Q9DHW0	Q9dhw0 yaba-like d
2	59.5	39.4	1238	12 Q9EMP3	Q9emp3 amasata moo
3	55.5	36.8	177	2 Q57377	Q57377 shigella fl
4	54	35.8	779	10 Q9MBA4	Q9mba4 oryza sativ
5	51	33.8	2340	5 Q97298	Q97298 plasmodium
6	50.5	33.4	156	12 Q89337	Q89337 african swi
7	50	33.1	285	2 Q92D79	Q92d79 rickettsia
8	50	33.1	440	5 Q9W478	Q9w478 drosophila
9	50	33.1	558	10 Q81052	Q81052 arabidopsis
10	50	33.1	721	2 Q86171	Q86171 clostridium
11	50	33.1	1150	3 Q43052	Q43052 schistosom
12	49.5	32.8	139	12 Q9YVVO	Q9yvvo melanopus
13	49.5	32.8	489	2 Q9CEA2	Q9cea2 lactococcus
14	49.5	32.8	489	5 Q9AZH2	Q9azh2 bacterioph
15	49.5	32.8	1148	5 Q17517	Q17517 caenorhabd
16	49	32.5	305	13 Q9W7E2	Q9w7e2 oryza sat
17	49	32.5	467	5 Q20265	Q20265 caenorhabd
18	49	32.5	558	10 Q9SWH5	Q9swh5 arabidopsis
19	49	32.5	1078	5 Q23326	Q23326 caenorhabd

20	48.5	32.1	293	2 Q50727	Q50727 borrelia bu
21	48.5	32.1	329	12 Q40852	Q40852 influenza a
22	48.5	32.1	779	2 Q94F36	Q94f36 bradyrhizob
23	48.5	32.1	1192	5 Q9W475	Q9w475 drosophila
24	48	31.8	275	2 Q51250	Q51250 borrelia bu
25	48	31.8	453	2 Q31049	Q31049 streptococ
26	47.5	31.5	148	5 Q9N339	Q9n339 caenorhabd
27	47.5	31.5	208	5 Q23373	Q23373 caenorhabd
28	47.5	31.5	347	5 Q23531	Q23531 caenorhabd
29	47.5	31.5	314	5 Q18860	Q18860 caenorhabd
30	47.5	31.5	314	5 Q9U3R4	Q9u3r4 caenorhabd
31	47.5	31.5	314	5 Q9TY50	Q9ty50 caenorhabd
32	47.5	31.5	329	12 Q40867	Q40867 influenza a
33	47.5	31.5	339	5 Q21759	Q21759 caenorhabd
34	47.5	31.5	339	5 Q01855	Q01855 caenorhabd
35	47.5	31.5	339	5 Q17225	Q17225 caenorhabd
36	47.5	31.5	339	5 Q17521	Q17521 caenorhabd
37	47.5	31.5	339	5 Q46640	Q46640 caenorhabd
38	47.5	31.5	339	5 Q18300	Q18300 caenorhabd
39	47.5	31.5	339	5 Q18360	Q18360 caenorhabd
40	47.5	31.5	339	5 Q17746	Q17746 caenorhabd
41	47.5	31.5	339	5 Q20886	Q20886 caenorhabd
42	47.5	31.5	339	5 Q21908	Q21908 caenorhabd
43	47.5	31.5	339	5 Q45860	Q45860 caenorhabd
44	47.5	31.5	339	5 Q9U359	Q9u359 caenorhabd
45	47.5	31.5	339	5 Q9U1V7	Q9u1v7 caenorhabd

ALIGNMENTS

RESULT 1

ID Q9DHW0 PRELIMINARY; PRT; 338 AA.

AC Q9DHW0: 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)

DE 2L PROTEIN PRECURSOR.

GN 2L.

OS Yaba-like disease virus.

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Yatapoxvirus.

OX NCBI_TaxID=132475;

RN [1]

RP SEQUENCE FROM N.A.

RA Lee H.-J., Smith G.L.;

RT "The genome sequence of Yaba-like disease virus, a yatapoxvirus.";

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Lee H.-J.;

RT Thesis (2000), Sir William Dunn School of Pathology, University of.

DR EMBL; AJ293568; CAC21240.1; -

DR InterPro; IPR003600; Ig-like.

DR SMART; SM00410; Ig-like; 1.

KW Signal.

ET SIGNAL.

SO SEQUENCE

Best Local Similarity 76.2%; Score 115; DB 12; Length 338;

Matches 22; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ITLKYCYVTLKNGLDGVFYCHYN 26

Db 17 ITLKYCYVTLKNGLDGVFYCHYN 42

RESULT 2

Q9EMP3 PRELIMINARY; PRT; 1238 AA.

STIC-ILL

From: Winkler, Ulrike
Sent: Tuesday, March 05, 2002 7:04 PM
To: STIC-ILL

STIC:
I would really like to get a copy of the following thesis for evaluation of PCT/US01/32136.

Thanks, Ulrike

Ulrike Winkler, Ph.D.
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REFERENCE 1 (bases 1 to 144575)

AUTHORS Lee,H.J.

JOURNAL Thesis (2000) Sir William Dunn School of Pathology, University of
Oxford, Oxford, UNITED KINGDOM

REFERENCE 2 (bases 1 to 144575)

AUTHORS Lee,H.J., Essani,K. and Smith,G.L.

TITLE The genome sequence of Yaba-like disease virus, a yatapoxvirus

JOURNAL Virology 281 (2), 170-192 (2001)

MEDLINE 21176366

REFERENCE 3 (bases 1 to 144575)

AUTHORS Lee,H.J.

TITLE Direct Submission

JOURNAL Submitted (13-JUL-2000) Lee H.J., Sir William Dunn School of
Pathology, University of Oxford, South Parks road, Oxford, OX1 3RE,
UNITED KINGDOM